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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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In re Application of: SIEGALL ET AL.

MAY 30 2001

Serial No.: 09/328,296

Examiner: K. Canella

TECH CENTER 1600/2900

Filed: June 8, 1999

Group Art Unit: 1642

For: RECOMBINANT ANTI-CD40 ANTIBODY  
AND USES THEREOF

Attorney Docket No.: 9632-005

#13

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6-12-01

**SUPPLEMENTAL RESPONSE UNDER 37 C.F.R. § 1.111**

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

To supplement and pursuant to the Amendment filed by Applicants on April 18, 2001 in connection with the above-identified application, Applicants submit herewith an original Declaration of Dr. Joseph A. Francisco under 37 C.F.R. § 1.132, which was executed by Dr. Joseph A. Francisco on April 27, 2001. An unexecuted counterpart of the enclosed Declaration was filed on April 18, 2001.

**REMARKS**

Applicants note that with respect to Exhibit Q of the Amendment filed on April 18, 2001, which contained sequence alignments of the heavy and light chain variable regions and complementarity determining regions of the anti-CD40 antibodies 5D12, humanized 5D12, and S2C6, the percentage sequence identities were calculated as follows: Each pair of sequences was aligned using the AlignX module of the sequence analysis program Vector NTI. AlignX is a sequence alignment program that utilizes the Clustal W algorithm (Thompson *et al.*, 1994, Nucleic Acids Res. 22(22):4673-80 and page 31, line 36 of the specification). The Clustal W algorithm assigns a "best fit" based on the identity and similarity of residues and allows for the insertion of gaps under defined criteria. After each pair of sequences was aligned using AlignX, the percentage of sequence identity for each pair was calculated by AlignX as the percentage of the sum of exact amino acid matches at